

1/8

GCGCCCGCGGTCTTCCCGAGGTTCTTAGGTCCTTCACTTCTGTTTGCCGGCACTTCAAAATCCGGGTCAAAGGGTG [SEQ ID NO:1]
TCGCTTCGGTCTCTTCTCCCCGGCTGATCCAGCACTCTCCGTGACAGCGCCTCCTGACTCAGCCAGGACCGGCTTCT
TCTCAGCACTGCTGGAGACTGGACGCCACACCTGACCCGGAACCTCGAGGGCTGCTTCTCCACCCGCCGGCTAGCA
GCCCCGGGCCCTGAGCTCCCGCCGACGCCGTGGGGGGCCGACAGGCCCTCGGCCTGATGCTGAGTGGGATCGAGG
GCCCCGGGGCGGGCGGAGTACGGGCCTCTGGCGCCTTAGGCCAGCCGAGGTGTCGGTTCTTAGGCTCTCCAGGCTCG
CTAGCTCCGCCCCGGCTTGGATGGGTCTCCCTGCCCATAAATGTGGCTGCTGAGCGGGCGGTGGCCGTGGCCCGTCG
CGCTGCTGCTGCGGCGCTCCAAGTTCATCTCGCCCCGGGGCTCTCCTGCCCCACCTCGGGGCTGCCGCCACCCGCTCC

M D K I L E G L V S S [SEQ ID NO: 2]
TTATCCCCTGGCCCTGGCCTTGACGCGTGGCGACA ATG GAC AAG ATC CTG GAG GGC CTT GTG AGT TCC 33
↑SEQ ID NO:3→

S H P L P L K R V I V R K V V E S A E H 31
TCG CAT CCC CTG CCC CTC AAG CGG GTG ATT GTG CGG AAG GTG GTG GAA TCG GCG GAG CAC 93
W L D E A Q C E A M F D L T T R L I L E 51
TGG CTA GAC GAG GCG CAG TGC GAG GCC ATG TTT GAC CTG ACG ACC CGG CTC ATC CTG GAG 153
G Q D P F Q R Q V G H Q V L E A Y A R Y 71
GGC CAG CAC CCT TTC CAG CGG CAG GTG GGG CAC CAG GTG CTG GAG GCC TAC GCA CGA TAC 213
H R P E F E S F F N K T F V L G L L H Q 91
CAC CGG CCA GAG TTC GAG TCC TTC TTC AAC AAG ACC TTC GTG TTG GGC CTC CTT CAT CAG 273
G Y H S L D R K D V A I L D Y I H N G L 111
GGC TAC CAC TCT CTG GAC AGG AAG GAT GTA GCC ATC CTG GAC TAC ATT CAC AAC GGC CTG 333

FIG. 1A

2/8

K L I M S C P S V L D L F S L L Q V E V 131
AAG CTG ATT ATG AGC TGT CCG TCG GTG CTG GAT CTC TTT AGC CTC CTG CAG GTA GAG GTG 393

L R M V C E R P E P Q L C A R L S D L L 151
TTA CCG ATG GTG TGT GAG AGG CCG GAG CCG CAG CTC TGT GCC CGA CTG AGC GAC CTT CTG 453

T D F V Q C I P K G K L S I T F C Q Q L 171
ACC GAC TTT GTG CAA TGC ATC CCC AAG GGG AAA TTG TCC ATC ACG TTC TGT CAA CAG CTG 513

V R T I G H F Q C V S T Q E R E L R E Y 191
GTT CGA ACG ATA GGC CAT TTC CAG TGC GTG TCC ACC CAG GAA AGA GAG CTG CGG GAA TAT 573

V S Q V T K V S N L L Q N I W K A E P A 211
GTC TCC CAG GTG ACA AAA GTG AGT AAC TTG CTG CAG AAC ATC TGG AAG GCC GAG CCT GCC 633

T L L P S L Q E V F A S I S S T D A S F 231
ACA CTA CTG CCT TCC CTG CAA GAA GTT TTT GCA AGC ATC TCT TCC ACA GAT GCA TCA TTT 693

E P S V A L A S L V Q H I P L Q M I T V 251
GAA CCT TCT GTA GCA TTG GCA AGC CTT GTG CAG CAT ATT CCT CTT CAG ATG ATT ACA GTT 753

L I R S L T T D P N V K D A S M T Q A L 271
CTC ATC AGG AGC CTT ACT ACG GAT CCA AAT GTA AAA GAT GCA AGT ATG ACC CAA GCC CTT 813

C R M I D W L S W P L A Q H V D T W V I 291
TGC AGA ATG ATT GAC TGG CTA TCC TGG CCA TTG GCT CAG CAT GTG GAT ACA TGG GTA ATT 873

A L L K G L A A V Q K F T I L I D V T L 311
GCA CTC CTG AAA GGA CTG GCA GCT GTC CAG AAG TTT ACT ATT TTG ATA GAT GTT ACT TTG 933

L K I E L V F N R L W F P L V R P G A L 331
CTG AAA ATA GAA CTG GTT TTT AAT CGA CTT TGG TTT CCT CTT GTG AGA CCT GGT GCT CTT 993

FIG. 1B

3/8

A V L S H M L L S F Q H S P E A F H L I 351
GCA GTT CTT TCT CAC ATG CTG CTT AGC TTT CAG CAT TCT CCA GAG GCG TTC CAT TTG ATT 1053

V P H V V N L V H S F K N D G L P S S T 371
GTT CCT CAT GTG GTT AAT TTG GTT CAT TCT TTC AAA AAT GAT GGT CTG CCT TCA AGT ACA 1113

A F L V Q L T E L I H C M M Y H Y S G F 391
GCC TTC TTA GTA CAA TTA ACA GAA TTG ATA CAC TGT ATG ATG TAT CAT TAT TCT GGA TTT 1173

P D L Y E P I L E A I K D F P K P S E E 411
CCA GAT CTC TAT GAA CCT ATT CTG GAG GCA ATA AAG GAT TTT CCT AAG CCC AGT GAA GAG 1233

K I K L I L N Q S A W T S Q S N S L A S 431
AAG ATT AAG TTA ATT CTC AAT CAA AGT GCC TGG ACT TCT CAA TCC AAT TCT TTG GCG TCT 1293

C L S R L S G K S E T G K T G L I N L G 451
TGC TTG TCT AGA CTT TCT GGA AAA TCT GAA ACT GGG AAA ACT GGT CTT ATT AAC CTA GGA 1353

N T C Y M N S V I Q A L F M A T D F R R 471
AAT ACA TGT TAT ATG AAC AGT GTT ATA CAA GCC TTG TTT ATG GCC ACA GAT TTC AGG AGA 1413

Q V L S L N L N G C N S L M K K L Q H L 491
CAA GTA TTA TCT TTA AAT CTA AAT GGG TGC AAT TCA TTA ATG AAA AAA TTA CAG CAT CTT 1473

F A F L A H T Q R E A Y A P R I F F E A 511
TTT GCC TTT CTG GCC CAT ACA CAG AGG GAA GCA TAC GCA CCT CGG ATA TTC TTT GAG GCT 1533

S R P P W F T P R S Q Q D C S E Y L R F 531
TCC AGA CCT CCA TGG TTT ACT CCC AGA TCA CAG CAA GAC TGT TCT GAA TAC CTC AGA TTT 1593

L L D R L H E E E K I L K V Q A S H K P 551
CTC CTT GAC AGG CTC CAT GAA GAA GAA AAG ATC TTG AAA GTT CAG GCC TCA CAC AAG CCT 1653

FIG. 1C

4/8

S E I L E C S E T S L Q E V A S K A A V 571
TCT GAA ATT CTG GAA TGC AGT GAA ACT TCT TTA CAG GAA GTA GCT AGT AAA GCA GCA GTA 1713

L T E T P R T S D G E K T L I E K M F G 591
CTA ACA GAG ACC CCT CGT ACA AGT GAC GGT GAG AAG ACT TTA ATA GAA AAA ATG TTT GGA 1773

G K L R T H I R C L N C R S T S Q K V E 611
GGA AAA CTA CGA ACT CAC ATA CGT TGT TTG AAC TGC AGG AGT ACC TCA CAA AAA GTG GAA 1833

A F T D L S L A F C P S S S L E N M S V 631
GCC TTT ACA GAT CTT TCG CTT GCC TTT TGT CCT TCC TCT TCT TTG GAA AAC ATG TCT GTC 1893

Q D P A S S P S I Q D G G L M Q A S V P 651
CAA GAT CCA GCA TCA TCA CCC AGT ATA CAA GAT GGT GGT CTA ATG CAA GCC TCT GTA CCC 1953

G P S E E P V V Y N P T T A A F I C D S 671
GGT CCT TCA GAA GAA CCA GTA GTT TAT AAT CCA ACA ACA GCT GCC TTC ATC TGT GAC TCA 2013

L V N E K T I G S P P N E F Y C S E N T 691
CTT GTG AAT GAA AAA ACC ATA GGC AGT CCT CCT AAT GAG TTT TAC TGT TCT GAA AAC ACT 2073

S V P N E S N K I L V N K D V P Q K P G 711
TCT GTC CCT AAC GAA TCT AAC AAG ATT CTT GTT AAT AAA GAT GTA CCT CAG AAA CCA GGA 2133

G E T T P S V T D L L N Y F L A P E I L 731
GGT GAA ACC ACA CCT TCA GTA ACT GAC TTA CTA AAT TAT TTT TTG GCT CCA GAG ATT CTT 2193

T G D N Q Y Y C E N C A S L Q N A E K T 751
ACT GGT GAT AAC CAA TAT TAT TGT GAA AAC TGT GCC TCT CTG CAA AAT GCT GAG AAA ACT 2253

M Q I T E E P E Y L I L T L L R F S Y D 771
ATG CAA ATC ACG GAG GAA CCT GAA TAC CTT ATT CTT ACT CTC CTG AGA TTT TCA TAT GAT 2313

FIG. 1D

5/8

Q K Y H V R R K I L D N V S L P L V L E 791
CAG AAG TAT CAT GTG AGA AGG AAA ATT TTA GAC AAT GTA TCA CTG CCA CTG GTT TTG GAG 2373

L P V K R I T S F S S L S E S W S V D V 811
TTG CCA GTT AAA AGA ATT ACT TCT TTC TCT TCA TTG TCA GAA AGT TGG TCT GTA GAT GTT 2433

D F T D L S E N L A K K L K P S G T D E 831
GAC TTC ACT GAT CTT AGT GAG AAC CTT GCT AAA AAA TTA AAG CCT TCA GGG ACT GAT GAA 2493

A S C T K L V P Y L L S S V V V H S G I 1851
GCT TCC TGC ACA AAA TTG GTG CCC TAT CTA TTA AGT TCC GTT GTG GTT CAC TCT GGT ATA 2553

S S E S G H Y Y S Y A R N I T S T D S S 871
TCC TCT GAA AGT GGG CAT TAC TAT TCT TAT GCC AGA AAT ATC ACA AGT ACA GAC TCT TCA 2613

Y Q M Y H Q S E A L A L A S S Q S H L L 891
TAT CAG ATG TAC CAC CAG TCT GAG GCT CTG GCA TTA GCA TCC TCC CAG AGT CAT TTA CTA 2673

G R D S P S A V F E Q D L E N K E M S K 911
GGG ACA GAT AGT CCC AGT GCA GTT TTT GAA CAG GAT TTG GAA AAT AAG GAA ATG TCA AAA 2733

E W F L F N D S R V T F T S F Q S V Q K 931
GAA TGG TTT TTA TTT AAT GAC AGT AGA GTG ACA TTT ACT TCA TTT CAG TCA GTC CAG AAA 2793

I T S R F P K D T A Y V L L Y K K Q H S 951
ATT ACG AGC AGG TTT CCA AAG GAC ACA GCT TAT GTG CTT TTG TAT AAA AAA CAG CAT AGT 2853

T N G L S G N N P T S G L W I N G D P P 971
ACT AAT GGT TTA AGT GGT AAT AAC CCA ACC AGT GGA CTC TGG ATA AAT GGA GAC CCA CCT 2913

L Q K E L M D A I T K D N K L Y L Q E Q 991
CTA CAG AAA GAA CTT ATG GAT GCT ATA ACA AAA GAC AAT AAA CTA TAT TTA CAC GAA CAA 2973

FIG. 1E

6/8

E L N A R A R A L Q A A S A S C S F R P 1011
GAG TTG AAT GCT CGA GCC CGG GCC CTC CAA GCT GCA TCT GCT TCA TGT TCA TTT CGG CCC 3033

N G F D D N D P P G S C G P T G G G G G 1031
AAT GGA TTT GAT GAC AAC GAC CCA CCA GGA AGC TGT GGA CCA ACT GGT GGA GGG GGT GGA 3093

G G F N T V G R L V F * 1043
GGA GGA TTT AAT ACA GTT GGC AGA CTC GTA TTT TGA 3129

←SEQ ID NO:3↑

TCCTGAGAGAGTCCAAAATGCACTGGTCACGAAACGTCTAATACTATGACTGTTAAAATGTCAGACTATAACAAATATC
TATCTTTTATTTTCATTAGACCCCTTATACTTCAAGAGAACACACTCAGTGCTTGTTTTATTTCTTGACACATTTAT
TAACAAAATGCATCATGGAAAAAATCTACCTCTTAAATTCATTGCTTTTATGGTTAGACATGCTTGACCAAAAA
TGTTGAGAAGAAATATGTACCTGGTCCCTAATTAAGCTGCGTTAAATTTGGTAGAAGCATTAAATGGTCTATCTTCA
GTTTTACTGAACAAAAATGTAATTTATTTAGCATTCTTTATAAAGAATTGATGCTAGAGGTAAAAAAATACTTGT
TTTTAAAAATCCTTTACGTCTTGTTAATTACCCCATTTATAAATCAAGTCCTTGAAATCAACTAGAGATTATAAA
GTCTCTAAGAAGGCAATAACAAAATTTATCAAGATATAGTACTTTTCAGTTTTTGTTTGTCTTCAGCATCACTGT
GTCTGTATTTCAAGTACAAATGTTTTTAAAAAGGATTCTTTATACATATGTGCTGAATTGATTTTAAGGAAAGTTGCAT
GATCCTGTAGGAGCAACATTTTACCTAAAAATGCTAACTTTATAGTATTTCTAATTGTTCAAGGATTTTAAATCT
GATCCTGTAGGAGCAACATTTTACCTAAAAATGCTAACTTTATAGTATTTCTAATTGTTCAAGGATTTTAAATCT

FIG. 1F

7/8

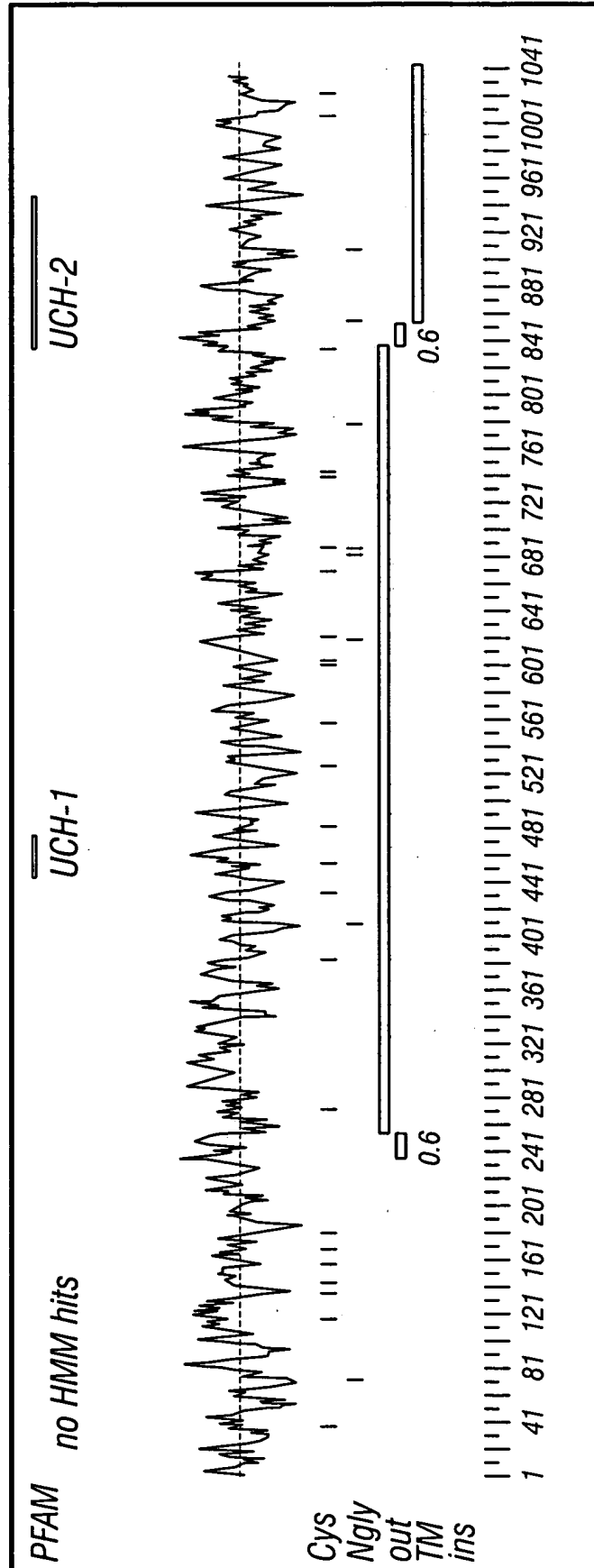


FIG. 2

8/8

->tGLiNlGNTCYmNSvLQcLfsipplrldylldi<- [SEQ ID NO:4]
 tGLiNlGNTCYmNSv+Q+Lf++ ++r+ +l++
 23430 445 TGLINLGNTCYMNSVIQALFMATDFRRQVLSL 476

FIG. 3

*->gpgkYeLyaVvvHsGsslsgGHYtayvkken..... [SEQ ID NO:5]
 + + Y L +VvvHsG s+ +GHY++y+++ +++++ + +++++
 23430 836 KLVPLYLLSSVVVHSGISSESGHYYSYARNITstdssyqmyhqseala 882
WykFDDdkVsrvteeavlke
 +++++ +++++ + +++++ +++++ +++++ +++++ +++++
 23430 883 lassqshllgrdpsavfeqdlenkemskeWFLFNDsrvtFTSFQSVQKI 932
 sggesgdtssAYiLfYer<-*
 + ++AY+L+Y++
 23430 923 TSR--FPKDTAYVLLYKK 948

FIG. 4

Query: 710 PGGETTPSVTDLLNYFLAPEILTGDNQYYCENCASLQNAEKTMQITEEPEYLILTLRFS 769
 P G+ + S+ D L F PE L GDN+Y+CE C Q+A K + I + P+ L + L RF
 Sbjct: 12 PEGDHS-SLEDCLEQFFKPEELEGDNKYHCEKCKKKQDATKQLTIKKLPQVLTiHLKRFE 70 [SEQ ID NO: 6]
 Query: 770 YDQTYHVRKILDMVSLPL-VLEL 792
 Y +++ KI +VS PL L+L
 Sbjct: 71 YMEERFSSNKINKHVSFPLETLDL 94

FIG. 5